

SEQUENCE LISTING

RADEMA

<120> BILIVERDIN REDUCTASE FRAGMENTS AND VARIANTS, AND METHODS OF USING BILIVERDIN REDUCTASE AND SUCH FRAGMENTS AND VARIANTS

<130> 176/60792

<140> 09/606,129

<141> 2000-06-28

<150> 60/141,309

<151> 1999-06-28

<150> 60/163,223

<151> 1999-11-03

<160> 37

<170> PatentIn Ver. 2.1

<210> 1

<211> 296

<212> PRT

<213> Homo sapiens

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Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
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Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu 35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser 50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu

100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp 130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp 145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu 165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu 195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys 210 225

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn 225 230 230 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn 245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala 260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile 275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys 290 295

<210> 2

<211> 1070

<212> DNA

<213> Homo sapiens

<400> 2

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<210> 3

<211> 296

<212> PRT

<213> Homo sapiens

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Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser 50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu 100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp

130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu 145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu 165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu 180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu 195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys 210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn 225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn 245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala 260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile 275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys 290 295

<210> 4

<211> 295

<212> PRT

<213> Rattus norvegicus

<400> 4

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Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser 20 25 30

Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly 35 40 45

- Ser Leu Asp Glu Val Arg Gln İle Ser Leu Glu Asp Ala Leu Arg Ser 50 55 60
- Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu 65 70 75 .80
- Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu 85 90 95
- Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu 100 105 110
- Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu 115 120 125
- Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu 130 135 140
- Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg
 145 150 155 160
- Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val 165 170 175
- Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg 180 185 190
- Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn 195 200 205
- Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg 210 215 220
- Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val 225 230 235 240
- Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile 245 250 255
- Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala 260 265 270
- Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln 275 280 285
- Lys Leu Cys His Gln Lys Lys 290 295

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tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct 360
graggetgge aagratgtee tegtggaata ecceatgaca etgteatttg eggeggeeca 420
ggagetgtgg gagetggeeg cacagaaagg gagagteetg catgaggage acgtggaact 480
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                                                                  1081
<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: hydrophobic
      domain of BVR
<220>
<221> PEPTIDE
<222> (2)
<223> where X is any aa
<400> 6
Phe Xaa Val Val Val
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<210> 7

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<211> 6
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: nucleotide
       binding domain of BVR
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 <221> PEPTIDE
 <222> (2)
 <223> where X is any aa
 <220>
 <221> PEPTIDE
 <222> (4)..(5)
 <223> where X is any aa
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 <210> 8
 <211> 8
 <212> PRT
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence:
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                   5
   1
 <210> 9
 <211> 29
 <212> PRT
 <213> Artificial Sequence
 <220>
<223> Description of Artificial Sequence: leucine
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 <220>
 <221> PEPTIDE
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<222> (2)..(7)
<223> where X is any aa
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<221> PEPTIDE
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<223> where X is any aa
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<222> (23)..(28)
<223> where X is any aa
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                  5
Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Leu
             20
                                 25
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<223> Description of Artificial Sequence: kinase motif
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<223> where X is any aa
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<212> PRT
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<400> 13
Gly Leu Lys Arg Asn Arg Tyr
 1
<210> 14
<211> 5
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: methylation
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<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: zinc finger
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<221> PEPTIDE
<222> (3)..(12)
<223> where X is any aa
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                                     10
<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: protein
     kinase C enhancing domain
<220>
<221> PEPTIDE
<222> (5)
<223> where X is any aa
<400> 16
Lys Lys Arg Ile Xaa His Cys
<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: protein
      kinase C inhibiting domain
<220>
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<222> (3)
<223> where X is any aa
<220>
<221> PEPTIDE
<222> (5)..(7)
<223> where X is any aa
<400> 17
Gln Lys Xaa Cys Xaa Xaa Xaa Lys
<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: protein
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<400> 18
Lys Lys Arg Ile Met His Cys
<210> 19
<211> 8
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: protein
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Gln Lys Leu Cys His Gln Lys Lys
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<211> 1014

<212> PRT

<213> Homo sapiens

<400> 20

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Gly Arg Ala Ser Cys Lys Lys Cys Ser Glu Ser Ile Pro Lys Asp Ser 20 25 30

Leu Arg Met Ala Ile Met Val Gln Ser Pro Met Phe Asp Gly Lys Val 35 40 45

Pro His Trp Tyr His Phe Ser Cys Phe Trp Lys Val Gly His Ser Ile 50 55 60

Arg His Pro Asp Val Glu Val Asp Gly Phe Ser Glu Leu Arg Trp Asp 65 70 75 80

Asp Gln Gln Lys Val Lys Lys Thr Ala Glu Ala Gly Gly Val Thr Gly 85 90 95

Lys Gly Gln Asp Gly Ile Gly Ser Lys Ala Glu Lys Thr Leu Gly Asp 100 105 110

Phe Ala Ala Glu Tyr Ala Lys Ser Asn Arg Ser Thr Cys Lys Gly Cys 115 120 125

Met Glu Lys Ile Glu Lys Gly Gln Val Arg Leu Ser Lys Lys Met Val 130 135 140

Asp Pro Glu Lys Pro Gln Leu Gly Met Ile Asp Arg Trp Tyr His Pro 145 150 155 160

Gly Cys Phe Val Lys Asn Arg Glu Glu Leu Gly Phe Arg Pro Glu Tyr 165 170 175

Ser Ala Ser Gln Leu Lys Gly Phe Ser Leu Leu Ala Thr Glu Asp Lys 180 185 190

Glu Ala Leu Lys Lys Gln Leu Pro Gly Val Lys Ser Glu Gly Lys Arg 195 200 205

Lys Gly Asp Glu Val Asp Gly Val Asp Glu Val Ala Lys Lys Ser 210 215 220

Lys Lys Glu Lys Asp Lys Asp Ser Lys Leu Glu Lys Ala Leu Lys Ala

225	230	235	240
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	245	250	255
Ser Thr Asn Asp L 260	-	Leu Ile Phe Asn Lys 265	Gln Gln Val
Pro Ser Gly Glu S	Ser Ala Ile Leu	Asp Arg Val Ala Asp	Gly Met Val
275	280	285	
Phe Gly Ala Leu L	eu Pro Cys Glu	Glu Cys Ser Gly Gln	Leu Val Phe
290	295	300	
Lys Ser Asp Ala T 305	Tyr Tyr Cys Thr	Gly Asp Val Thr Ala 315	Trp Thr Lys
-	Thr Gln Thr Pro . 325	Asn Arg Lys Glu Trp 330	Val Thr Pro
Lys Glu Phe Arg G	_	Leu Lys Lys Leu Lys 345	Val Lys Lys 350
Gln Asp Arg Ile P	Phe Pro Pro Glu 9	Thr Ser Ala Ser Val	Ala Ala Thr
355	360	365	
Pro Pro Pro Ser T	Thr Ala Ser Ala	Pro Ala Ala Val Asn	Ser Ser Ala
370	375	380	
Ser Ala Asp Lys P	Pro Leu Ser Asn 1	Met Lys Ile Leu Thr	Leu Gly Lys
385	390	395	400
	Lys Asp Glu Val :	Lys Ala Met Ile Glu	Lys Leu Gly
	105	410	415
Gly Lys Leu Thr G	-	Lys Ala Ser Leu Cys	Ile Ser Thr
420		425	430
Lys Lys Glu Val G	Slu Lys Met Asn	Lys Lys Met Glu Glu	Val Lys Glu
435	440	445	
Ala Asn Ile Arg V	Val Val Ser Glu .	Asp Phe Leu Gln Asp	Val Ser Ala
450	455	460	
Ser Thr Lys Ser L	Leu Gln Glu Leu	Phe Leu Ala His Ile	Leu Ser Pro
465	470	475	480

Trp Gly Ala Glu Val Lys Ala Glu Pro Val Glu Val Val Ala Pro Arg

				485					490					495	
Gly	Lys	Ser	Gly 500	Ala	Ala	Leu	Ser	Lys 505	Lys	Ser	Lys	Gly	Gln 510	Val	Lys
Glu	Glu	Gly 515	Ile	Asn	Lys	Ser	Glu 520	Lys	Arg	Met	Lys	Leu 525	Thr	Leu	Lys
Gly	Gly 530	Ala	Ala	Val	Asp	Pro 535	Asp	Ser	Gly	Leu	Glu 540	His	Ser	Ala	His
Val 545	Leu	Glu	Lys	Gly	Gly 550	Lys	Val	Phe	Ser	Ala 555	Thr	Leu	Gly	Leu	Val 560
Asp	Ile	Val	Lys	Gly 565	Thr	Asn	Ser	Tyr	Tyr 570	Lys	Leu	Gln	Leu	Leu 575	Glu
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Asp	Ala 610	Ile	Glu	His	Phe	Met 615	Lys	Leu	Tyr	Glu	Glu 620	Lys	Thr	Gly	Asn
Ala 625	Trp	His	Ser	Lys	Asn 630	Phe	Thr	Lys	Tyr	Pro 635	Lys	Lys	Phe	Tyr	Pro 640
Leu	Glu	Ile	Asp	Tyr 645	Gly	Gln	Asp	Glu	Glu 650	Ala	Val	Lys	Lys	Leu 655	Thr
Val	Asn	Pro	Gly 660	Thr	Lys	Ser	Lys	Leu 665	Pro	Lys	Pro	Val	Gln 670	Asp	Leu
Ile	Lys	Met 675	Ile	Phe	Asp	Val	Glu 680	Ser	Met	Lys	Lys	Ala 685	Met	Val	Glu
Tyr	Glu 690	Ile	Asp	Leu	Gln	Lys 695	Met	Pro	Leu	Gly	Lys 700	Leu	Ser	Lys	Arg

Ser Gln Gly Ser Ser Asp Ser Gln Ile Leu Asp Leu Ser Asn Arg Phe
725 730 735

Gln Ile Gln Ala Ala Tyr Ser Ile Leu Ser Glu Val Gln Gln Ala Val

715

710

705

Tyr Thr Leu Ile Pro His Asp Phe Gly Met Lys Lys Pro Pro Leu Leu

Asn Asn Ala Asp Ser Val Gln Ala Lys Val Glu Met Leu Asp Asn Leu Leu Asp Ile Glu Val Ala Tyr Ser Leu Leu Arg Gly Gly Ser Asp Asp Ser Ser Lys Asp Pro Ile Asp Val Asn Tyr Glu Lys Leu Lys Thr Asp Ile Lys Val Val Asp Arg Asp Ser Glu Glu Ala Glu Ile Ile Arg Lys Tyr Val Lys Asn Thr His Ala Thr Thr His Asn Ala Tyr Asp Leu Glu Val Ile Asp Ile Phe Lys Ile Glu Arg Glu Gly Glu Cys Gln Arg Tyr Lys Pro Phe Lys Gln Leu His Asn Arg Arg Leu Leu Trp His Gly Ser Arg Thr Thr Asn Phe Ala Gly Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly Ile Tyr Phe Ala Asp Met Val Ser Lys Ser Ala Asn Tyr Cys His Thr Ser Gln Gly Asp Pro Ile Gly Leu Ile Leu Leu Gly Glu Val Ala Leu Gly Asn Met Tyr Glu Leu Lys His Ala Ser His Ile Ser Lys Leu Pro Lys Gly Lys His Ser Val Lys Gly Leu Gly Lys Thr Thr Pro Asp Pro Ser Ala Asn Ile Ser Leu Asp Gly Val Asp Val Pro Leu Gly Thr Gly Ile Ser

- 965 970 975
- Ser Gly Val Asn Asp Thr Ser Leu Leu Tyr Asn Glu Tyr Ile Val Tyr 980 985 990
- Asp Ile Ala Gln Val Asn Leu Lys Tyr Leu Leu Lys Leu Lys Phe Asn

995 1000 1005

Phe Lys Thr Ser Leu Trp 1010

<210> 21 <211> 3660 <212> DNA <213> Homo sapiens

<400> 21

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25

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1 5	
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